

Romeo

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1646

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/945,459A

DATE: 11/02/98
TIME: 11:40:25

INPUT SET: S29578.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

- (i) APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU,
HIROYUKI; MIKI, HIDEO; KAWAI,
SHINJI; KIMURA, MICHIO; MATSUMOTO,
TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
KOICHI; SATOH, YUSUKE
- (ii) TITLE OF INVENTION: A NOVEL PROTEIN AND
PROCESS FOR PREPARING THE SAME
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
LLP
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: MICROSOFT WORD 97
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/945,459
(B) FILING DATE: 09-DEC-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP96/01062
(B) FILING DATE: 19-APR-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP7/322403
(B) FILING DATE: 17-NOV-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP7/93664
(B) FILING DATE: 19-APR-1995

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47 (vii) ATTORNEY/AGENT INFORMATION:
48
49
50
51
52
53
54 (A) NAME: CHARLES A. MUSERLIAN
55 (B) REGISTRATION NUMBER: 19,683
56 (C) REFERENCE/DOCKET NUMBER: 146.1275
57
58 (ix) TELECOMMUNICATION INFORMATION:
59 (A) TELEPHONE: (212) 661-8000
60 (B) TELEFAX: (212) 661-8002
61 (C) TELEX:
62
63
64 (2) INFORMATION FOR SEQ ID NO:1:
65
66 (i) SEQUENCE CHARACTERISTICS:
67 (A) LENGTH: 119 AMINO ACIDS
68 (B) TYPE: AMINO ACID
69 (C) STRANDEDNESS:
70 (D) TOPOLOGY: LINEAR
71
72 (ii) MOLECULE TYPE: PEPTIDE
73
74 (vi) ORIGINAL SOURCE:
75 (A) ORGANISM: HOMOSAPIENS
76 (F) TISSUE TYPE: FETUS
77
78 (ix) FEATURE:
79 (A) NAME/KEY: MP52
80 (B) LOCATION: 383 TO 501
81
82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
83
84 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys
85 1 5 10
86
87 Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu His
88 15 20
89
90 Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile
91 25 30 35
92
93 Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
94 40 45
95
96 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu
97 50 55 60
98
99 Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn

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100
101
102
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107
108 Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys
109 75 80
110
111 Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
112 85 90 95
113
114 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr
115 100 105
116
117 Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg
118 110 115
119
120
121 (2) INFORMATION FOR SEQ ID NO:2:
122
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 27 BASE PAIRS
125 (B) TYPE: NUCLEIC ACID
126 (C) STRANDEDNESS: SINGLE
127 (D) TOPOLOGY: LINEAR
128
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
130
131 ATAATGCCAC TAGCAACTCG TCAGGGC 27
132
133
134 (2) INFORMATION FOR SEQ ID NO:3:
135
136 (i) SEQUENCE CHARACTERISTICS:
137 (A) LENGTH: 26 BASE PAIRS
138 (B) TYPE: NUCLEIC ACID
139 (C) STRANDEDNESS: SINGLE
140 (D) TOPOLOGY: LINEAR
141
142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
143
144 CGTCGACTAC CTGCAGCCAC ACGACT 26
145
146
147 (2) INFORMATION FOR SEQ ID NO:4:
148
149 (i) SEQUENCE CHARACTERISTICS:
150 (A) LENGTH: 357 BASE PAIRS
151 (B) TYPE: NUCLEIC ACID
152 (C) STRANDEDNESS: DOUBLE

RAW SEQUENCE LISTING PATENT APPLICATION US/08/945,459A

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(D) TOPOLOGY: UNKNOWN

153

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

162

163 CCA CTG GCC ACT CGC CAG GGC AAG CGA CCC AGC AAG 36

164 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys

165 1 5 10

166

167 AAC CTT AAG GCT CGC TGC AGT CGG AAG GCA CTG CAT 72

168 Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu His

169 15 20

170

171 GTC AAC TTC AAG GAC ATG GGC TGG GAC GAC TGG ATC 108

172 Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile

173 25 30 35

174

175 ATC GCA CCC CTT GAG TAC GAG GCT TTC CAC TGC GAG 144

176 Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu

177 40 45

178

179 GGG CTG TGC GAG TTC CCA TTG CGC TCC CAC CTG GAG 180

180 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu

181 50 55 60

182

183 CCC ACG AAT CAT GCA GTC ATC CAG ACC CTG ATG AAC 216

184 Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn

185 65 70

186

187 TCC ATG GAC CCC GAG TCC ACA CCA CCC ACC TGC TGT 252

188 Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys

189 75 80

190

191 GTG CCC ACG CGA CTG AGT CCC ATC AGC ATC CTC TTC 288

192 Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe

193 85 90 95

194

195 ATT GAC TCT GCC AAC AAC GTG GTG TAT AAG CAG TAT 324

196 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr

197 100 105

198

199 GAG GAC ATG GTC GTG GAG TCG TGT GGC TGC AGG 357

200 Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg

201 110 115

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SEQUENCE VERIFICATION REPORT
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Original Text